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RAW SEQUENCE LISTING　　　　　　DATE: 07/15/2002
PATENT APPLICATION: US/10/049,187　　TIME: 12:38:09

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   3 <110> APPLICANT: CHOI, YANG-DO
   4         CHEONG, JONG-JOO
   5         LEE, JONG-SEOB
   6         SONG, JONG-TAE
   7         SONG, SANG-IK
   8         SEO, HAK-SOO
   9         KOO, YEON-JONG
  11 <120> TITLE OF INVENTION: GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID
  12         CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE
  13         DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS
  14         USING THE GENES
  16 <130> FILE REFERENCE: 058333/0112
  18 <140> CURRENT APPLICATION NUMBER: 10/049,187
C--> 19 <141> CURRENT FILING DATE: 2002-06-13
  21 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00953
  22 <151> PRIOR FILING DATE: 2001-06-05
  24 <160> NUMBER OF SEQ ID NOS: 8
  26 <170> SOFTWARE: PatentIn Ver. 2.1
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  29 <211> LENGTH: 1170
  30 <212> TYPE: DNA
  31 <213> ORGANISM: Arabidopsis thaliana
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  35 aactccaccg ctcagagcaa cataatatct ctaggcagaa gagtaatgga cgaggccttg 120
  36 aagaagttaa tgatgagcaa ttcagagatt tcgagcattg gaatcgccga cttaggctgc 180
  37 tcctccggtc cgaacagtct cttgtccatc tccaacatag ttgacacgat ccacaacttg 240
  38 tgtcctgacc tcgaccgtcc agtccctgag ctcagagtct ctctcaacga cctccctagc 300
  39 aatgacttca actacatatg tgcttctttg ccagagtttt acgaccgggt taataataac 360
  40 aaggagggtt tagggttcgg tcgtggagga ggagaatcgt gttttgtgtc ggccgtccca 420
  41 ggttcgttct acggacgttt gtttcctcgc cggagccttc actttgtgca ttcttcttct 480
  42 agtttacatt ggttgtctca ggttccatgt cgtgaggcgg agaaggaaga caggacaata 540
  43 acagctgatt agaaaacat ggggaaaata tacatatcaa agacaagtcc taagagtgca 600
  44 cataaagctt atgctcttca attccaaact gatttcttgg ttttttttgag gtcacgatct 660
  45 gaggagttgg tcccgggagg ccgaatggtt ttatcgttcc ttggtagaag atcactggat 720
  46 cccacaaccg aagagagttg ctatcaatgg gaactcctag ctcaagctct tatgtccatg 780
  47 gccaaagagg gtatcatcga ggaagagaag atcgatgctt caacgctcc ttactatgct 840
  48 gcgagctccg aagagttgaa aatggtgata gagaagaag ggtcattttc gatcgatagg 900
  49 cttgagataa gtccgattga ttgggaaggt gggagtatca gtgaggagag ttatgacctt 960
  50 gcaataaggt ccaaacccga gccctagct agtggccgaa gagtgtctaa taccataaga 1020
  51 gctgtggtcg agccgatgct agaacctact ttcggtgaaa atgtgatgga cgagctttt 1080
  52 gaaaggtatg caaagatcgt gggagagtac ttctatgtaa gctcgccacg atacgctatt 1140
  53 gttattcttt cgctcgttag aaccggttga                                    1170
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63 <222> LOCATION: (15)..(1181)
64 <223> OTHER INFORMATION: open reading frame for JMT
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68                  Met Glu Val Met Arg Val Leu His Met Asn Lys Gly
69                   1               5                  10
71 aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac ata     98
72 Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile
73         15                  20                  25
75 ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg    146
76 Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met
77     30                  35                  40
79 atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc    194
80 Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys
81  45                  50                  55                  60
83 tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg    242
84 Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr
85                  65                  70                  75
87 atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc aga    290
88 Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg
89             80                  85                  90
91 gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt gct    338
92 Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala
93         95                  100                 105
95 tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta    386
96 Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu
97     110                 115                 120
99 ggg ttc ggt cgt gga gga gga gaa tcg tgt ttt gtg tcg gcc gtc cca    434
100 Gly Phe Gly Arg Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro
101 125                 130                 135                 140
103 ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg   482
104 Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val
105                 145                 150                 155
107 cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt gag   530
108 His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu
109             160                 165                 170
111 gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg   578
112 Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly
113         175                 180                 185
115 aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct tat   626
116 Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr
117     190                 195                 200
119 gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga tct   674
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120 Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser
121 205             210             215             220
123 gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt aga  722
124 Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg
125             225             230             235
127 aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc  770
128 Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu
129             240             245             250
131 cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag gaa  818
132 Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu
133      .   255             260             265
135 gag aag atc gat gct ttc aac gct cct tac tat gct gcg agc tcc gaa  866
136 Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu
137     270             275             280
139 gag ttg aaa atg gtg ata gag aaa gaa ggg tca ttt tcg atc gat agg  914
140 Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg
141 285             290             295             300
143 ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag  962
144 Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu
145             305             310             315
147 agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc 1010
148 Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly
149             320             325             330
151 cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa 1058
152 Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu
153             335             340             345
155 cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca 1106
156 Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala
157     350             355             360
159 aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att 1154
160 Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile
161 365             370             375             380
163 gtt att ctt tcg ctc gtt aga acc ggt tgatcgtgtt ataacatatg      1201
164 Val Ile Leu Ser Leu Val Arg Thr Gly
165             385
167 ccaatataca tgtctttggg cctacaatga catgatttgg tagttttcta atcaagcata 1261
169 tgtaatataa tttgcttcga gaataaaata ataaataaa gtgtgatgtt acggtagacc 1321
171 cttttttttt tttcttcatt tacggtagac ctatagtatt aaaacaaata gaatcagctg 1381
173 gttcggacct tgaaatgaga gagcttggat gcatgtagac gcattagtcg tgaattattc 1441
175 aaatagaact accttttggg ccaaaaaaaa aaaaa                         1476
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 389
180 <212> TYPE: PRT
181 <213> ORGANISM: Arabidopsis thaliana
183 <400> SEQUENCE: 3
184 Met Glu Val Met Arg Val Leu His Met Asn Lys Gly Asn Gly Glu Thr
185   1             5             10             15
187 Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile Ile Ser Leu Gly
188             20             25             30
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190 Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
191         35              40              45
193 Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
194         50              55              60
196 Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
197 65              70              75              80
199 Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
200             85              90              95
202 Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
203             100             105             110
205 Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
206         115             120             125
208 Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
209     130             135             140
211 Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
212 145             150             155             160
214 Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
215             165             170             175
217 Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
218         180             185             190
220 Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
221         195             200             205
223 Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
224     210             215             220
226 Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
227 225             230             235             240
229 Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
230             245             250             255
232 Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
233         260             265             270
235 Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
236         275             280             285
238 Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
239     290             295             300
241 Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
242 305             310             315             320
244 Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
245             325             330             335
247 Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
248         340             345             350
250 Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
251     355             360             365
253 Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
254 370             375             380
256 Leu Val Arg Thr Gly
257 385
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 30
262 <212> TYPE: DNA
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263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' primer for
267   PCR of JMT gene
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270 cgcgtccgaa ttcgagagag agagaatgga   30
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 30
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' primer for
280   PCR of JMT gene
282 <400> SEQUENCE: 5
283 tttgaagaat tcacgactaa tgcgtctaca   30
286 <210> SEQ ID NO: 6
287 <211> LENGTH: 359
288 <212> TYPE: PRT
289 <213> ORGANISM: Clarkia breweri
291 <400> SEQUENCE: 6
292 Met Asp Val Arg Gln Val Leu His Met Lys Gly Gly Ala Gly Glu Asn
293   1   5   10   15
295 Ser Tyr Ala Met Asn Ser Phe Ile Gln Arg Gln Val Ile Ser Ile Thr
296   20   25   30
298 Lys Pro Ile Thr Glu Ala Ala Ile Thr Ala Leu Tyr Ser Gly Asp Thr
299   35   40   45
301 Val Thr Thr Arg Leu Ala Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
302   50   55   60
304 Asn Ala Leu Phe Ala Val Thr Glu Leu Ile Lys Thr Val Glu Glu Leu
305   65   70   75   80
307 Arg Lys Lys Met Gly Arg Glu Asn Ser Pro Glu Tyr Gln Ile Phe Leu
308   85   90   95
310 Asn Asp Leu Pro Gly Asn Asp Phe Asn Ala Ile Phe Arg Ser Leu Pro
311   100   105   110
313 Ile Glu Asn Asp Val Asp Gly Val Cys Phe Ile Asn Gly Val Pro Gly
314   115   120   125
316 Ser Phe Tyr Gly Arg Leu Phe Pro Arg Asn Thr Leu His Phe Ile His
317   130   135   140
319 Ser Ser Tyr Ser Leu Met Trp Leu Ser Gln Val Pro Ile Gly Ile Glu
320 145   150   155   160
322 Ser Asn Lys Gly Asn Ile Tyr Met Ala Asn Thr Cys Pro Gln Ser Val
323   165   170   175
325 Leu Asn Ala Tyr Tyr Lys Gln Phe Gln Glu Asp His Ala Leu Phe Leu
326   180   185   190
328 Arg Cys Arg Ala Gln Glu Val Val Pro Gly Gly Arg Met Val Leu Thr
329   195   200   205
331 Ile Leu Gly Arg Arg Ser Glu Asp Arg Ala Ser Thr Glu Cys Cys Leu
332   210   215   220
334 Ile Trp Gln Leu Leu Ala Met Ala Leu Asn Gln Met Val Ser Glu Gly

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L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date